Application No. 10/699,393 Response Dated October 24, 2006 Reply to Office Action of August 24, 2006

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Exhibit A

The invention Shows Synergistic Results (From Tables 1 and 2, see Specification, pages 48 and 50)

Property	E217A	W215A	WE
PA/FC *	40.06	170	2865
Fibrinogen k _{cat/} K _m (μM ⁻¹ s ⁻¹)	0.27	0.034	0.00089
Fibrin k _{cat/} K _m (μM ⁻¹ s ⁻¹)	0.15	0.053	0.0021
Protein C + TM k _{cat} /K _m (µM ⁻¹ s ⁻¹)	0.14	0.075	0.033
PAR1 k _{cat} /K _m (µM ⁻¹ s ⁻¹)	0.66	1	0.026
Antithrombin III kon (µM ⁻¹ s ⁻¹) ^d	1	0.56	0.0040

^{*}The PA/FC here are calculated from the data shown in Tables 1 and 2. The term "PA/FC ratio" as used herein refers to the ratio of the percent of wild-type protein C activation (PA) activity remaining in a thrombin variant relative to the percent of wild-type fibrinogen clotting (FC) activity remaining in the thrombin variant. A value of PA/FC greater than 1.0 indicates that the thrombin variant has reduced procoagulant fibrinogen cleavage activity relative to the residual anticoagulant activity resulting from protein C activation. See Specification 16.

Comparative Data Between Cited References and the Invention

Property	The Primary Reference E229A (E217A)	The Secondary Reference W215A	The Invention WE
PA/FC *	19.1	170	2865

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ARTICLE

An Allosteric Switch Controls the Procoagulant and Anticoagulant **Activities of Thrombin**

OD Dang, A Vindigni and ED Cera.

Thrombin is an allosteric enzyme existing in two forms, slow and fast, that differ widely in their specificities toward synthetic and natural amide substrates. The two forms are significantly populated in vivo, and the allosteric equilibrium can be affected by the binding of effectors and natural substrates. The fast form is procoagulant because it cleaves fibrinogen with higher specificity; the slow form is anticoagulant because it cleaves protein C with higher specificity. Binding of thrombomodulin inhibits cleavage of fibrinogen by the fast form and promotes cleavage of protein C by the slow form. The allosteric properties of thrombin, which has targeted two distinct conformational

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states toward its two fundamental and competing roles in hemostasis, are paradigmatic of a molecular strategy that is likely to be exploited by other proteases in the blood coagulation cascade.

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Biochemistry and Molecular Biology International

Publisher: Taylor & Francis

Issue: Volume 44, Number 1 / January 1998

Pages: 175 - 183

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DOI: 10.1080/15216549800201192

Non-synergistic interactions between strong allosteric effectors and human embryonic and adult haemoglobins

Amy, E.M. McLennan A1 and Thomas Brittain A1

A1 Biochemistry and Molecular Biology School of Biological Sciences, University of Auckland, Auckland, New Zealand

Abstract:

The binding of two strong allosteric effectors (2,3 Diphosphoglycerate D.P.G., and Bezafibrate, Bzf) to both adult and the three human embryonic haemoglobins, either individually or in combination, have been studied in detail. The adult protein exhibits one binding site for D.P.G and two for Bzf. When both effectors are present simultaneously their effects are simply additive. The same qualitative pattern of binding is observed in the case of the three human embryonic haemoglobins, although with different binding constants. The lack of synergism between these effectors and the different binding affinity expressed by these proteins are discussed in terms of the known amino acid sequence differences.

Keywords:

haemoglobin, embryonic, allosteric, effectors

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Kinetic Characterization of a T-State of Ascaris



suumPhosphofructokinase with **Heterotropic Negative Cooperativity** by ATP Eliminated

Authors: Jagannatha Rao G.S.1; Cook P.F.2; Harris B.G.1

Source: Archives of Biochemistry and Biophysics, Volume 365, Number 2, May 1999, pp. 335-343(9)

Publisher: Academic Press

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Abstract:

The affinity analogue, 2',3'-dialdehyde ATP has been used to chemically modify the ATP-inhibitory site of Ascaris suumphosphofructokinase, thereby locking the enzyme into a less active T-state. This enzyme form has a maximum velocity that is 10% that of the native enzyme in the direction of fructose 6phosphate (F6P) phosphorylation. The enzyme displays sigmoid saturation for the substrate fructose 6phosphate $(S_{0.5}(F6P) = 19 \text{ mM} \text{ and } n_H = 2.2)$ at pH 6.8 and a hyperbolic saturation curve for MgATP with aKmidentical to that for the native enzyme. The allosteric effectors, fructose 2,6-bisphosphate and AMP, do not affect the S_{0.5} for F6P but produce a slight (1.5- and 2-fold, respectively) V-type activation

with Kavalues (effector concentration required for half-maximal activation) of 0.40 and 0.24 mM, respectively. Their activating effects are additive and not synergistic. The kinetic mechanism for the modified enzyme is steady-state-ordered with MgATP as the first substrate and MgADP as the last product to be released from the enzyme surface. The decrease InVandV/Kvalues for the reactants likely results from a decrease in the equilibrium constant for the isomerization of the E:MgATP binary complex, thus favoring an unisomerized form. TheVandV/K_{F6P} are pH dependent with similar pKvalues of about 7 on the acid side and 9.8 on the basic side. The microenvironment of the active site appears to be affected minimally as evidenced by the similarity of the pKvalues for the groups involved in the binding site for F6P in the modified and native enzymes.Copyright 1999 Academic Press.

Keywords: Ascaris suum; phosphofructokinase; T-state; R-state; dialdehyde-ATP; V-type activation; allosteric effectors

Language: English

Document Type: Research article

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